

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/574,306A
Source: IFWP
Date Processed by STIC: 3/15/07

ENTERED



IFWP

RAW SEQUENCE LISTING DATE: 03/15/2007
PATENT APPLICATION: US/10/574,306A TIME: 15:06:51

Input Set : A:\50458.002001.txt
Output Set: N:\CRF4\03152007\J574306A.raw

3 <110> APPLICANT: Korherr, Christian
5 <120> TITLE OF INVENTION: Medical Use of TBK-1 or of Inhibitors Thereof
7 <130> FILE REFERENCE: 50458/002001
9 <140> CURRENT APPLICATION NUMBER: US 10/574,306A
10 <141> CURRENT FILING DATE: 2006-04-03
12 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/010996
13 <151> PRIOR FILING DATE: 2004-10-01
15 <150> PRIOR APPLICATION NUMBER: US 60/508,100
16 <151> PRIOR FILING DATE: 2003-10-02
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3031
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
28 cctcgtgccg aattcggcac gaggccgc ggcgggtggcg cggcggagac ccggctggta 60
30 taacaagagg attgcctgat ccagccaaga tgcagagcac ttctaattcat ctgtggctt 120
32 tatctgatat tttaggc当地 ggaactactg caaatgtt tcgtggaa cataagaaaa 180
34 ctggtgattt atttgctatc aaagtattta ataacataag cttccttcgt ccagtgatg 240
36 ttcaaatgag agaatttcaa gtgttggaaa aactcaatca caaaaatattt gtcaaattat 300
38 ttgttattga agaggagaca acaacaagac ataaagtact tattatggaa ttttgc当地 360
40 gtgggagttt atacactgtt ttagaagaac cttctaattgc ctatggacta ccagaatctg 420
42 aattcttaat tggtttgc当地 gatgtgggtgg gtggaatgaa tcatctacga gagaatggta 480
44 tagtgcaccg tgatataaag ccaggaaata tcatgc当地 tataggggaa gatggacagt 540
46 ctgtgtacaa actcacagat ttgggtgc当地 cttagagaatt agaagatgat gagcagttt 600
48 ttctctgtt tggcacagaa gaatatttgc accctgatat gtatggagaga gcagtgctaa 660
50 gaaaagatca tcagaagaaa tatggagca cagttgatct ttggagcatt ggggtaacat 720
52 ttaccatgc agtacttggaa tcactgc当地 tttagaccctt tgaagggccct cgttagaata 780
54 aagaagtgtt gtataaaaata attacaggaa agccttctgg tgcaatatct ggagtacaga 840
56 aagcagaaaaa tggaccaatt gactggagtg gagacatgcc tggcttgc agtcttctc 900
58 ggggtcttca gggtctactt acccctgttcc ttgcaaacat ccttgaagca gatcaggaaa 960
60 agtggggggg ttttgaccag ttttttgc当地 aaactagtga tataatttc当地 cgaatggtaa 1020
62 ttcatgtttt ttgc当地 taaaatgc当地 ctcataagat ttatattcat agtataata 1080
64 ctgtactat atttcatgaa ctgttatata aacaaacca aatttatttc当地 tcaaataag 1140
66 aacttatcta cgaaggccgaa cgcttagtct tagaacctgg aaggctggca caacattcc 1200
68 ctaaaaactac tgagggaaaac cctatatttgc tagtaagccg ggaacctctg aataccatag 1260
70 gattaatata tgaaaaaatttcccttccctt aagtacatcc acgttatgat ttagacgggg 1320
72 atgcttagcat ggcttaaggca ataacaggggg ttgtgttta tgcctgc当地 attgc当地 1380
74 ccttactgct ttatcagaa ttaatgc当地 aggggatacg atggctgattt gaattaatta 1440
76 aagatgatta caatgaaact gttcacaaaaa agacagaagt tggatcaca ttggatttct 1500
78 gtatcagaaa cattgaaaaa actgtgaaag tatatgaaaaa gttgatgaaatcaacctgg 1560
80 aagccggc当地 gtttaggtgaa atttc当地 gacacccaa attqttqaa ctttccqattt 1620

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82	ctcagggAAC	aatagaaACC	agtcttcAGG	atatcgACAG	cagattatCT	ccaggtGGAT	1680
84	caactggCAGA	cgccatgggCA	catcaagaAGA	gcactcatCC	gaaagacAGA	aatgttagAAA	1740
86	aactacaAGT	cctgttaAAAT	tgcataGACAG	agattactA	tcagttCAA	aaagacAAAG	1800
88	cagaacgtAG	attagcttAT	aatgaagaACAC	aaatccacAA	atttgataAG	caaaaaactGT	1860
90	attaccatGC	cacaaaAGCT	atgacgcACT	ttacagatGA	atgtgttAA	aagtatGAGG	1920
92	cattttgAA	taagtcaGAA	gaatggataAA	gaaagatGCT	tcatcttAGG	aaacagttAT	1980
94	tatcgctGAC	taatcaGtGT	tttgatattG	aagaagaAGT	atcaaaataAT	caagaatATA	2040
96	ctaataGAGTT	acaagaaACT	ctgcctcAGA	aaatgttAC	agcttccAGT	ggaatcaAAc	2100
98	ataccatGAC	cccaatttat	ccaaGttcTA	acacattAGT	agaaaatGACT	cttggtatGA	2160
100	agaaaattAA	ggaagagatG	gaaggggTGG	ttaaagaACT	tgctgaaaAT	aaccacattT	2220
102	tagaaaggTT	tggctttaA	accatggATG	gtggccttCG	caacgttGAC	tgtctttAGC	2280
104	tttctaataG	aagttaAGA	aaagtttCCG	tttgcacaAG	aaaataacGC	ttgggcatta	2340
106	aatgaatGcc	tttataGata	gtcacttGTT	tctacaattC	agtatttGAT	gtggcgtGT	2400
108	aaatatgtAC	aatattgtAA	atacataAAA	aatatacAA	ttttggctG	ctgtgaAGAT	2460
110	gtatattttAT	cttttaacAT	ttataattAT	atgaggAA	ttgacctcAG	tgatcacGAG	2520
112	aagaaaagCCA	tgaccgacCA	atatgttGAC	atactgatCC	tctactctGA	gtggggctAA	2580
114	ataagttattT	ttctctgacc	gcctactGGA	aatattttA	agtggAACCA	aaataggGCAT	2640
116	ccttacaaAT	caggaagact	gacttgacAC	gtttgtAA	ggtagaacGG	tggctactGT	2700
118	gagtggggAG	cagaaccgCA	ccactgttAT	actggataAA	caatttttT	gagaaggATA	2760
120	aagtggcattT	attttatttT	acaagggtGCC	cagatcccAG	ttatccttGT	atccatgtAA	2820
122	tttcagatGA	attattaAGC	aaacatttA	aagtgaattC	attattaaaa	actattcatt	2880
124	ttttccTT	ggccataat	gtgttaattG	cattaaaATT	ctaaggcAt	ttcaactgtT	2940
126	ttaagctgtA	tatttcttA	attctgcttA	ctatttcatG	gaaaaaaATA	aatttctcaa	3000
128	tttaatgtA	aagaaaaaaa	aaaaaaaaaa	a			3031

131 <210> SEQ ID NO: 2

132 <211> LENGTH: 729

133 <212> TYPE: PRT

134 <213> ORGANISM: Homo sapiens

136 <400> SEQUENCE: 2

138	Met	Gln	Ser	Thr	Ser	Asn	His	Leu	Trp	Leu	Leu	Ser	Asp	Ile	Leu	Gly
139	1						5			10					15	
142	Gln	Gly	Ala	Thr	Ala	Asn	Val	Phe	Arg	Gly	Arg	His	Lys	Lys	Thr	Gly
143							20			25				30		
146	Asp	Leu	Phe	Ala	Ile	Lys	Val	Phe	Asn	Asn	Ile	Ser	Phe	Leu	Arg	Pro
147							35			40				45		
150	Val	Asp	Val	Gln	Met	Arg	Glu	Phe	Glu	Val	Leu	Lys	Lys	Leu	Asn	His
151							50			55			60			
154	Lys	Asn	Ile	Val	Lys	Leu	Phe	Ala	Ile	Glu	Glu	Glu	Thr	Thr	Arg	
155							65			70			75		80	
158	His	Lys	Val	Leu	Ile	Met	Glu	Phe	Cys	Pro	Cys	Gly	Ser	Leu	Tyr	Thr
159							85			90			95			
162	Val	Leu	Glu	Glu	Pro	Ser	Asn	Ala	Tyr	Gly	Leu	Pro	Glu	Ser	Glu	Phe
163							100			105			110			
166	Leu	Ile	Val	Leu	Arg	Asp	Val	Val	Gly	Gly	Met	Asn	His	Leu	Arg	Glu
167							115			120			125			
170	Asn	Gly	Ile	Val	His	Arg	Asp	Ile	Lys	Pro	Gly	Asn	Ile	Met	Arg	Val
171							130			135			140			
174	Ile	Gly	Glu	Asp	Gly	Gln	Ser	Val	Tyr	Lys	Leu	Thr	Asp	Phe	Gly	Ala
175	145						145			150			155		160	

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178 Ala Arg Glu Leu Glu Asp Asp Glu Gln Phe Val Ser Leu Tyr Gly Thr
179 165 170 175
182 Glu Glu Tyr Leu His Pro Asp Met Tyr Glu Arg Ala Val Leu Arg Lys
183 180 185 190
186 Asp His Gln Lys Lys Tyr Gly Ala Thr Val Asp Leu Trp Ser Ile Gly
187 195 200 205
190 Val Thr Phe Tyr His Ala Ala Thr Gly Ser Leu Pro Phe Arg Pro Phe
191 210 215 220
194 Glu Gly Pro Arg Arg Asn Lys Glu Val Met Tyr Lys Ile Ile Thr Gly
195 225 230 235 240
198 Lys Pro Ser Gly Ala Ile Ser Gly Val Gln Lys Ala Glu Asn Gly Pro
199 245 250 255
202 Ile Asp Trp Ser Gly Asp Met Pro Val Ser Cys Ser Leu Ser Arg Gly
203 260 265 270
206 Leu Gln Val Leu Leu Thr Pro Val Leu Ala Asn Ile Leu Glu Ala Asp
207 275 280 285
210 Gln Glu Lys Cys Trp Gly Phe Asp Gln Phe Phe Ala Glu Thr Ser Asp
211 290 295 300
214 Ile Leu His Arg Met Val Ile His Val Phe Ser Leu Gln Gln Met Thr
215 305 310 315 320
218 Ala His Lys Ile Tyr Ile His Ser Tyr Asn Thr Ala Thr Ile Phe His
219 325 330 335
222 Glu Leu Val Tyr Lys Gln Thr Lys Ile Ile Ser Ser Asn Gln Glu Leu
223 340 345 350
226 Ile Tyr Glu Gly Arg Arg Leu Val Leu Glu Pro Gly Arg Leu Ala Gln
227 355 360 365
230 His Phe Pro Lys Thr Thr Glu Glu Asn Pro Ile Phe Val Val Ser Arg
231 370 375 380
234 Glu Pro Leu Asn Thr Ile Gly Leu Ile Tyr Glu Lys Ile Ser Leu Pro
235 385 390 395 400
238 Lys Val His Pro Arg Tyr Asp Leu Asp Gly Asp Ala Ser Met Ala Lys
239 405 410 415
242 Ala Ile Thr Gly Val Val Cys Tyr Ala Cys Arg Ile Ala Ser Thr Leu
243 420 425 430
246 Leu Leu Tyr Gln Glu Leu Met Arg Lys Gly Ile Arg Trp Leu Ile Glu
247 435 440 445
250 Leu Ile Lys Asp Asp Tyr Asn Glu Thr Val His Lys Lys Thr Glu Val
251 450 455 460
254 Val Ile Thr Leu Asp Phe Cys Ile Arg Asn Ile Glu Lys Thr Val Lys
255 465 470 475 480
258 Val Tyr Glu Lys Leu Met Lys Ile Asn Leu Glu Ala Ala Glu Leu Gly
259 485 490 495
262 Glu Ile Ser Asp Ile His Thr Lys Leu Leu Arg Leu Ser Ser Ser Gln
263 500 505 510
266 Gly Thr Ile Glu Thr Ser Leu Gln Asp Ile Asp Ser Arg Leu Ser Pro
267 515 520 525
270 Gly Gly Ser Leu Ala Asp Ala Trp Ala His Gln Glu Gly Thr His Pro
271 530 535 540
274 Lys Asp Arg Asn Val Glu Lys Leu Gln Val Leu Leu Asn Cys Met Thr

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275	545	550	555	560
278	Glu Ile Tyr Tyr Gln Phe Lys Lys Asp Lys Ala Glu Arg Arg Leu Ala			
279	565	570	575	
282	Tyr Asn Glu Glu Gln Ile His Lys Phe Asp Lys Gln Lys Leu Tyr Tyr			
283	580	585	590	
286	His Ala Thr Lys Ala Met Thr His Phe Thr Asp Glu Cys Val Lys Lys			
287	595	600	605	
290	Tyr Glu Ala Phe Leu Asn Lys Ser Glu Glu Trp Ile Arg Lys Met Leu			
291	610	615	620	
294	His Leu Arg Lys Gln Leu Leu Ser Leu Thr Asn Gln Cys Phe Asp Ile			
295	625	630	635	640
298	Glu Glu Glu Val Ser Lys Tyr Gln Glu Tyr Thr Asn Glu Leu Gln Glu			
299	645	650	655	
302	Thr Leu Pro Gln Lys Met Phe Thr Ala Ser Ser Gly Ile Lys His Thr			
303	660	665	670	
306	Met Thr Pro Ile Tyr Pro Ser Ser Asn Thr Leu Val Glu Met Thr Leu			
307	675	680	685	
310	Gly Met Lys Lys Leu Lys Glu Glu Met Glu Gly Val Val Lys Glu Leu			
311	690	695	700	
314	Ala Glu Asn Asn His Ile Leu Glu Arg Phe Gly Ser Leu Thr Met Asp			
315	705	710	715	720
318	Gly Gly Leu Arg Asn Val Asp Cys Leu			
319	725			
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323	<211> LENGTH: 19			
324	<212> TYPE: RNA			
325	<213> ORGANISM: artificial			
327	<220> FEATURE:			
328	<223> OTHER INFORMATION: oligonucleotide siTBK-1 sense			
330	<400> SEQUENCE: 3			
331	ggagacaaca acaagacau		19	
334	<210> SEQ ID NO: 4			
335	<211> LENGTH: 20			
336	<212> TYPE: RNA			
337	<213> ORGANISM: artificial			
339	<220> FEATURE:			
340	<223> OTHER INFORMATION: oligonucleotide siTBK-1 antisense			
342	<400> SEQUENCE: 4			
343	augucuuguu guugucucc		20	
346	<210> SEQ ID NO: 5			
347	<211> LENGTH: 23			
348	<212> TYPE: DNA			
349	<213> ORGANISM: artificial			
351	<220> FEATURE:			
352	<223> OTHER INFORMATION: oligonucleotide TBK-1 sense			
354	<400> SEQUENCE: 5			
355	ttgaagagga gacaacaaca aga		23	
358	<210> SEQ ID NO: 6			
359	<211> LENGTH: 19			

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360 <212> TYPE: DNA
361 <213> ORGANISM: artificial
363 <220> FEATURE:
364 <223> OTHER INFORMATION: oligonucleotide TBK-1 antisense
366 <400> SEQUENCE: 6
367 cattccaccc accacatct 19
370 <210> SEQ ID NO: 7
371 <211> LENGTH: 20
372 <212> TYPE: DNA
373 <213> ORGANISM: artificial
375 <220> FEATURE:
376 <223> OTHER INFORMATION: oligonucleotide VEGF sense
378 <400> SEQUENCE: 7
379 ctgccttgc tgctctacct 20
382 <210> SEQ ID NO: 8
383 <211> LENGTH: 20
384 <212> TYPE: DNA
385 <213> ORGANISM: artificial
387 <220> FEATURE:
388 <223> OTHER INFORMATION: oligonucleotide VEGF antisense
390 <400> SEQUENCE: 8
391 gattctgccc tcctccttct 20
394 <210> SEQ ID NO: 9
395 <211> LENGTH: 20
396 <212> TYPE: DNA
397 <213> ORGANISM: artificial
399 <220> FEATURE:
400 <223> OTHER INFORMATION: oligonucleotide Rantes sense
402 <400> SEQUENCE: 9
403 cgctgtcatc ctcattgcta 20
406 <210> SEQ ID NO: 10
407 <211> LENGTH: 20
408 <212> TYPE: DNA
409 <213> ORGANISM: artificial
411 <220> FEATURE:
412 <223> OTHER INFORMATION: oligonucleotide Rantes antisense
414 <400> SEQUENCE: 10
415 gcacttgcca ctgggttaga 20

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10

VERIFICATION SUMMARY

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